

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/594,908
Source: IFWP
Date Processed by STIC: 10/12/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 10/12/2006

PATENT APPLICATION: US/10/594,908

TIME: 14:03:47

Input Set : E:\SEQLIST 11774-006 (as filed).TXT

Output Set: N:\CRF4\10122006\J594908.raw

4 <110> APPLICANT: Wang, Xiangbin
 5 Huang, Hualiang
 6 Zhao, Baofeng
 7 Zhao, Qi
 8 Piao, Jinhua
 9 Lin, Qing
 11 <120> TITLE OF INVENTION: A GENETIC ENGINEERING RECOMBINANT ANTI-CEA, ANTI-
 CD3
 12 AND ANTI-CD28 SINGLE-CHAIN TRI-SPECIFIC ANTIBODY
 14 <130> FILE REFERENCE: 11774-006-999 (I040179)
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/594,908
 C--> 16 <141> CURRENT FILING DATE: 2006-09-29
 16 <150> PRIOR APPLICATION NUMBER: PCT/CN2005/000408
 17 <151> PRIOR FILING DATE: 2005-03-29
 19 <150> PRIOR APPLICATION NUMBER: CN 200410032158.3
 20 <151> PRIOR FILING DATE: 2004-04-01
 22 <160> NUMBER OF SEQ ID NOS: 58
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 251
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Murine
 31 <220> FEATURE:
 32 <223> OTHER INFORMATION: murine anti-CEA single chain fragment of variable
 region
 33 contained in CEA-scTsAb
 35 <400> SEQUENCE: 1
 36 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met Lys Pro Gly Ala
 37 1 5 10 15
 38 Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr Phe Ser Asp Tyr
 39 20 25 30
 40 Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp Ile
 41 35 40 45
 42 Gly Glu Ile Leu Pro Gly Ser Gly Arg Thr Asp Tyr Asn Glu Arg Phe
 43 50 55 60
 44 Lys Gly Lys Ala Thr Phe Thr Gly Asp Val Ser Ser Asn Thr Ala Tyr
 45 65 70 75 80
 46 Met Lys Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 47 85 90 95
 48 Ala Thr Gly Thr Thr Pro Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val
 49 100 105 110
 50 Thr Val Ser Ala Thr Ser Thr Pro Ser His Asn Ser His Gln Val Pro
 51 115 120 125
 52 Ser Ala Gly Gly Pro Thr Ala Asn Ser Gly Ser Arg Asp Ile Val Leu

53

130

135

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54 Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
55 145                      150                      155                      160
56 Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser Ser Tyr Thr Tyr
57                      165                      170                      175
58 Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
59                      180                      185                      190
60 Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
61                      195                      200                      205
62 Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
63          210                      215                      220
64 Glu Asp Thr Ala Tyr Tyr Tyr Cys Gln His Ser Trp Glu Ile Pro Arg
65 225                      230                      235                      240
66 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
67          245                      250

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70 <210> SEQ ID NO: 2

71 <211> LENGTH: 250

72 <212> TYPE: PRT

73 <213> ORGANISM: Murine

75 <220> FEATURE:

76 <223> OTHER INFORMATION: murine anti-CEA single chain fragment of variable region

77 contained in CEA-scTsAb

79 <400> SEQUENCE: 2

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80 Glu Val Lys Leu Val Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
81 1                      5                      10                      15
82 Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr
83          20                      25                      30
84 Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Met
85          35                      40                      45
86 Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe
87          50                      55                      60
88 Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
89 65                      70                      75                      80
90 Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
91          85                      90                      95
92 Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp
93          100                     105                     110
94 Gly Ala Gly Thr Ser Val Thr Val Ser Ser Thr Ser Gly Gly Gly Gly
95          115                     120                     125
96 Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Arg Asp Ile Gln
97          130                     135                     140
98 Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
99 145                      150                      155                      160
100 Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp
101          165                      170                      175
102 Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr
103          180                      185                      190
104 Ser Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser
105          195                      200                      205
106 Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile

```

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107      210      215      220
108 Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala
109 225      230      235      240
110 Gly Gly Thr Lys Leu Glu Leu Lys Arg Ala
111      245      250
114 <210> SEQ ID NO: 3
115 <211> LENGTH: 2103
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
120 <223> OTHER INFORMATION: CEA-scTsAb sequence
122 <400> SEQUENCE: 3
123 atgggtctcg agcagggtgca gctgcagcag agcgggtgcgg aactgatgaa accggggcgcg 60
124 agcgtgaaaa tcagctgcaa agcgaccggc tataccttca gcgattattg gatcgaatgg 120
125 gtgaaacagc gtccgggtca cggcctggaa tggatcgggtg aaatcctgcc gggcagcggc 180
126 cgtaccgact acaacgaacg tttcaaaggc aaagcgacct tcaccggcga cgtttctagc 240
127 aacaccgcgt atatgaaact gtctagcctg accagcgaaag atagcgcggt gtattactgc 300
128 gcgaccggca ccaccccggt cggttactgg ggtcagggca ccctggttac cgtttccgcg 360
129 actagtaccc cgagccataa cagccatcag gtgccgagcg cgggcggccc gaccgcgaac 420
130 agcgggtcta gagacatcgt gctgaccag agcccggcga gcctggcggt gtctctgggt 480
131 cagcgtgcga ccatctcctg ccgtgcttcc cagtccgttt ccacctctc ctacacctac 540
132 atgcactggg atcagcagaa accgggtcag ccgccgaaac tgctgatcaa atatgcgagc 600
133 aacctggaat ctggtgtgcc ggcgcgtttc agcggttctg gcagcggcac cgacttcacc 660
134 ctgaacatcc acccggtgga agaagaagat accgcgtatt actattgcca gcactcttgg 720
135 gaaatccgcg gtaccttcgg tggcggcacc aaactggaaa tcaaagaatt caacagcacg 780
136 taccgggttg taagcgctct caccgtactg caccaggact ggctgaatgg caaggaatac 840
137 aaatgcaaga gtactgaggt gaagctgggt gagtctggac ctgagctggg gaagcctgga 900
138 gcttcaatga agatatcctg caaggcttct ggttactcat tcaactggct caccatgaac 960
139 tgggtgaagc agagtcatgg aaagaacctt gagtggatgg gacttattaa tccttacaaa 1020
140 ggtgttagta cctacaacca gaagttcaag gacaaggcca cattaactgt agacaagtca 1080
141 tccagcacag cctacatgga actcctcagt ctgacatctg aggactctgc agtctattac 1140
142 tgtgcaagat cgggggtacta cggtgatagt gactggtagt tcgatgtctg gggcgcagga 1200
143 acctcagtcg ctgtctcctc aactagtggg ggtggtggtt ctggtggtgg tggttctggt 1260
144 ggtggtggtt cttctagaga catccagatg acccagacca catcctccct gtctgcctct 1320
145 ctggggagaca gagtcaccat cagttgcagg gcaagtcagg acattagaaa ttattttaaac 1380
146 tgggtatcaac agaaaccaga tggaaactgt aaactcctga tctactacac atcaagatta 1440
147 cactcaggag tcccatcaaa gttcagtggc agtgggtctg gaacagatta ttctctcacc 1500
148 attagcaacc tggagcaaga ggatattgcc acttactttt gccaacaggg taatacgctt 1560
149 ccgtggacgt tcgctggagg caccaaaactg gaactgaagc gcgctgtcga cttccagaat 1620
150 gcgctgctgg ttcgttacac caagaaagta ccccaagtgt caactccaac tcctgtagag 1680
151 gtctcacata tgcaggtaga gctacaggaa tctgggtccg gtctggtaaa accgtctcag 1740
152 accctgtctc tgacctgtac cgtatctggg ttctctctgt ctgactatgg tgttcattgg 1800
153 gtacgtcagc cgccaggtaa aggtctggaa tgtctgggtg taatatgggg tggaggcacg 1860
154 aattataatt cggctctcat gtccagacgt gtaacctctt ccgacgatac ctctaaaaat 1920
155 cagttctctc tgaaactgtc ttccgtagac accgctgtat actattgtgc tcgttcctat 1980
156 tactattcta tggactactg gggtcagggc accctggtaa ccgtatcttc cggtagccgaa 2040
157 caaaaactca tctcagaaga ggatctgaat ggggccgcac atcatcatca ccatcacgag 2100
158 caa 2103
160 <210> SEQ ID NO: 4

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161 <211> LENGTH: 701
162 <212> TYPE: PRT
163 <213> ORGANISM: Artificial Sequence
165 <220> FEATURE:
166 <223> OTHER INFORMATION: CEA-scTsAb sequence
168 <400> SEQUENCE: 4
169 Met Gly Leu Glu Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Met
170 1 5 10 15
171 Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Thr Gly Tyr Thr
172 20 25 30
173 Phe Ser Asp Tyr Trp Ile Glu Trp Val Lys Gln Arg Pro Gly His Gly
174 35 40 45
175 Leu Glu Trp Ile Gly Glu Ile Leu Pro Gly Ser Gly Arg Thr Asp Tyr
176 50 55 60
177 Asn Glu Arg Phe Lys Gly Lys Ala Thr Phe Thr Gly Asp Val Ser Ser
178 65 70 75 80
179 Asn Thr Ala Tyr Met Lys Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala
180 85 90 95
181 Val Tyr Tyr Cys Ala Thr Gly Thr Thr Pro Phe Gly Tyr Trp Gly Gln
182 100 105 110
183 Gly Thr Leu Val Thr Val Ser Ala Thr Ser Thr Pro Ser His Asn Ser
184 115 120 125
185 His Gln Val Pro Ser Ala Gly Gly Pro Thr Ala Asn Ser Gly Ser Arg
186 130 135 140
187 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
188 145 150 155 160
189 Gln Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
190 165 170 175
191 Ser Tyr Thr Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
192 180 185 190
193 Lys Leu Leu Ile Lys Tyr Ala Ser Asn Leu Glu Ser Gly Val Pro Ala
194 195 200 205
195 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
196 210 215 220
197 Pro Val Glu Glu Glu Asp Thr Ala Tyr Tyr Tyr Cys Gln His Ser Trp
198 225 230 235 240
199 Glu Ile Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Glu
200 245 250 255
201 Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
202 260 265 270
203 Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Ser Thr Glu Val Lys
204 275 280 285
205 Leu Val Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Met Lys
206 290 295 300
207 Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Gly Tyr Thr Met Asn
208 305 310 315 320
209 Trp Val Lys Gln Ser His Gly Lys Asn Leu Glu Trp Met Gly Leu Ile
210 325 330 335
211 Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn Gln Lys Phe Lys Asp Lys

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212          340          345          350
213 Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu
214          355          360          365
215 Leu Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Ser
216          370          375          380
217 Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe Asp Val Trp Gly Ala Gly
218 385          390          395          400
219 Thr Ser Val Thr Val Ser Ser Thr Ser Gly Gly Gly Gly Ser Gly Gly
220          405          410          415
221 Gly Gly Ser Gly Gly Gly Gly Ser Ser Arg Asp Ile Gln Met Thr Gln
222          420          425          430
223 Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser
224          435          440          445
225 Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln
226          450          455          460
227 Lys Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu
228 465          470          475          480
229 His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp
230          485          490          495
231 Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr
232          500          505          510
233 Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly Thr
234          515          520          525
235 Lys Leu Glu Leu Lys Arg Ala Val Asp Phe Gln Asn Ala Leu Leu Val
236          530          535          540
237 Arg Tyr Thr Lys Lys Val Pro Gln Val Ser Thr Pro Thr Pro Val Glu
238 545          550          555          560
239 Val Ser His Met Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val
240          565          570          575
241 Lys Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Phe Ser
242          580          585          590
243 Leu Ser Asp Tyr Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly
244          595          600          605
245 Leu Glu Cys Leu Gly Val Ile Trp Gly Gly Gly Thr Asn Tyr Asn Ser
246          610          615          620
247 Ala Leu Met Ser Arg Arg Val Thr Ser Ser Asp Asp Thr Ser Lys Asn
248 625          630          635          640
249 Gln Phe Ser Leu Lys Leu Ser Ser Val Asp Thr Ala Val Tyr Tyr Cys
250          645          650          655
251 Ala Arg Ser Tyr Tyr Tyr Ser Met Asp Tyr Trp Gly Gln Gly Thr Leu
252          660          665          670
253 Val Thr Val Ser Ser Gly Thr Glu Gln Lys Leu Ile Ser Glu Glu Asp
254          675          680          685
255 Leu Asn Gly Ala Ala His His His His His His Glu Gln
256          690          695          700
259 <210> SEQ ID NO: 5
260 <211> LENGTH: 18
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/594,908

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Input Set : E:\SEQLIST 11774-006 (as filed).TXT

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L:16 M:270 C: Current Application Number differs, Replaced Current Application No

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date